

Figure 1: Full-length Sequence of *C. pneumoniae* 76kDa Gene.

ataaaatctt taaaaacagg ctgcattaa ttattagtga gagctttttt tttatttttt 60

ataataaaac taaaagattt ttattatttt ttgagttttt atg gtt aat cct att 115  
Met Val Asn Pro Ile  
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163  
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu  
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211  
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala  
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259  
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp  
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307  
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met  
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355  
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser  
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403  
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr  
90 95 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451  
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala  
105 110 115

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct 499  
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala  
120 125 130

ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct 547  
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala  
135 140 145

act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc 595  
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala  
150 155 160 165

gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct 643  
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala  
170 175 180

tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc 691  
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe  
185 190 195

1004630444

Figure 1 (continued)

gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	
caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345 350 355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360 365 370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375 380 385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390 395 400 405	
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410 415 420	

10014670-121401

Figure 1 (continued)

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425 430 435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct	1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro	
440 445 450	
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag	1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys	
455 460 465	
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt	1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly	
470 475 480 485	
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat	1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn	
490 495 500	
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca	1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr	
505 510 515	
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca	1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr	
520 525 530	
gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga	1747
Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly	
535 540 545	
gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc	1795
Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile	
550 555 560 565	
cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca	1843
Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr	
570 575 580	
tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt	1891
Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu	
585 590 595	
tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt	1939
Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe	
600 605 610	
gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa	1987
Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu	
615 620 625	
acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta	2035
Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu	
630 635 640 645	

## Figure 1 (continued)

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 2083  
Tyr Ser Gly Tyr Leu Gln  
650

ttattatgtg ctttggttaag gcctttgttg aggccttacc aacacactag aacgatcttc 2143

aataaataaa aga 2156



Figure 2 (continued)

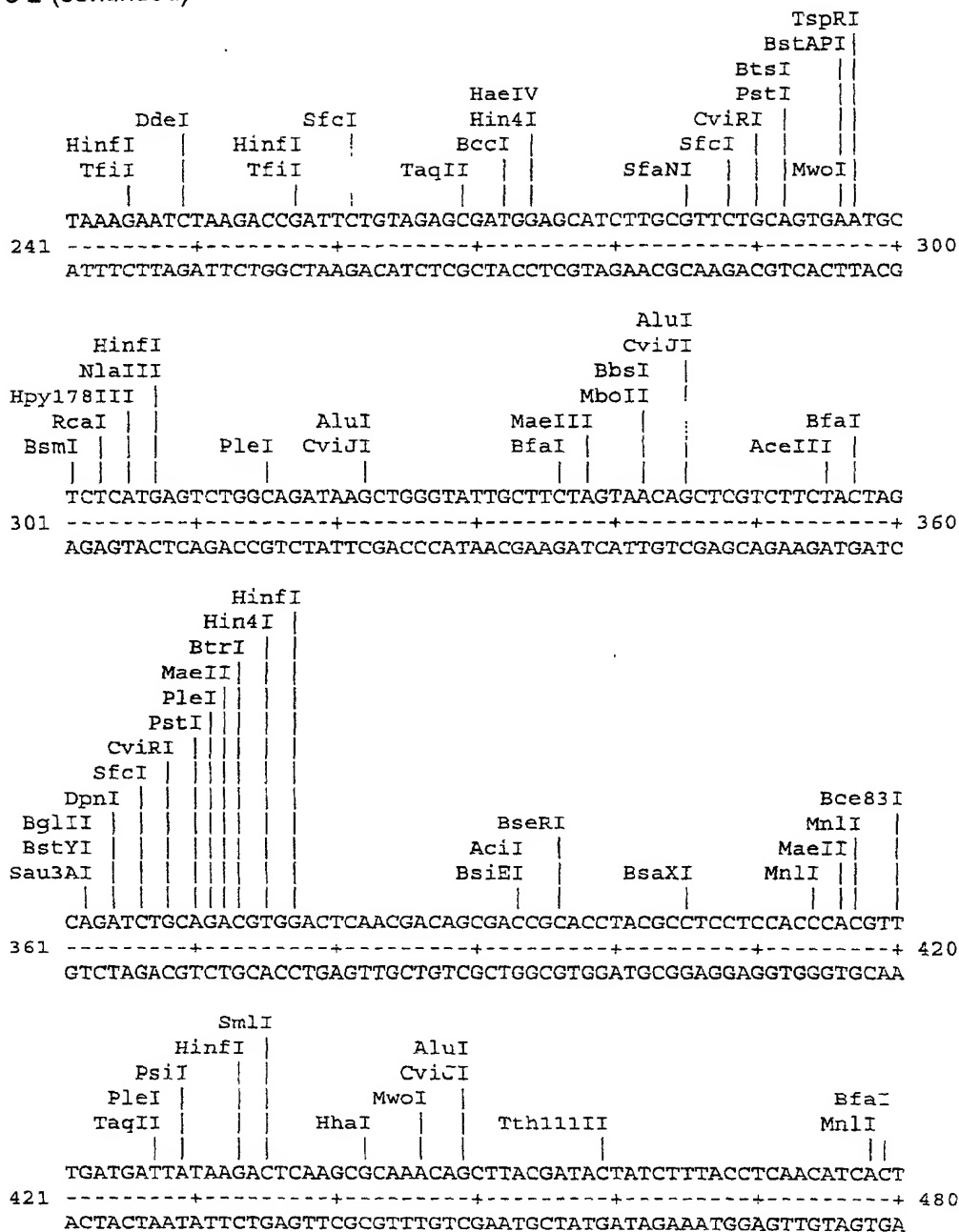
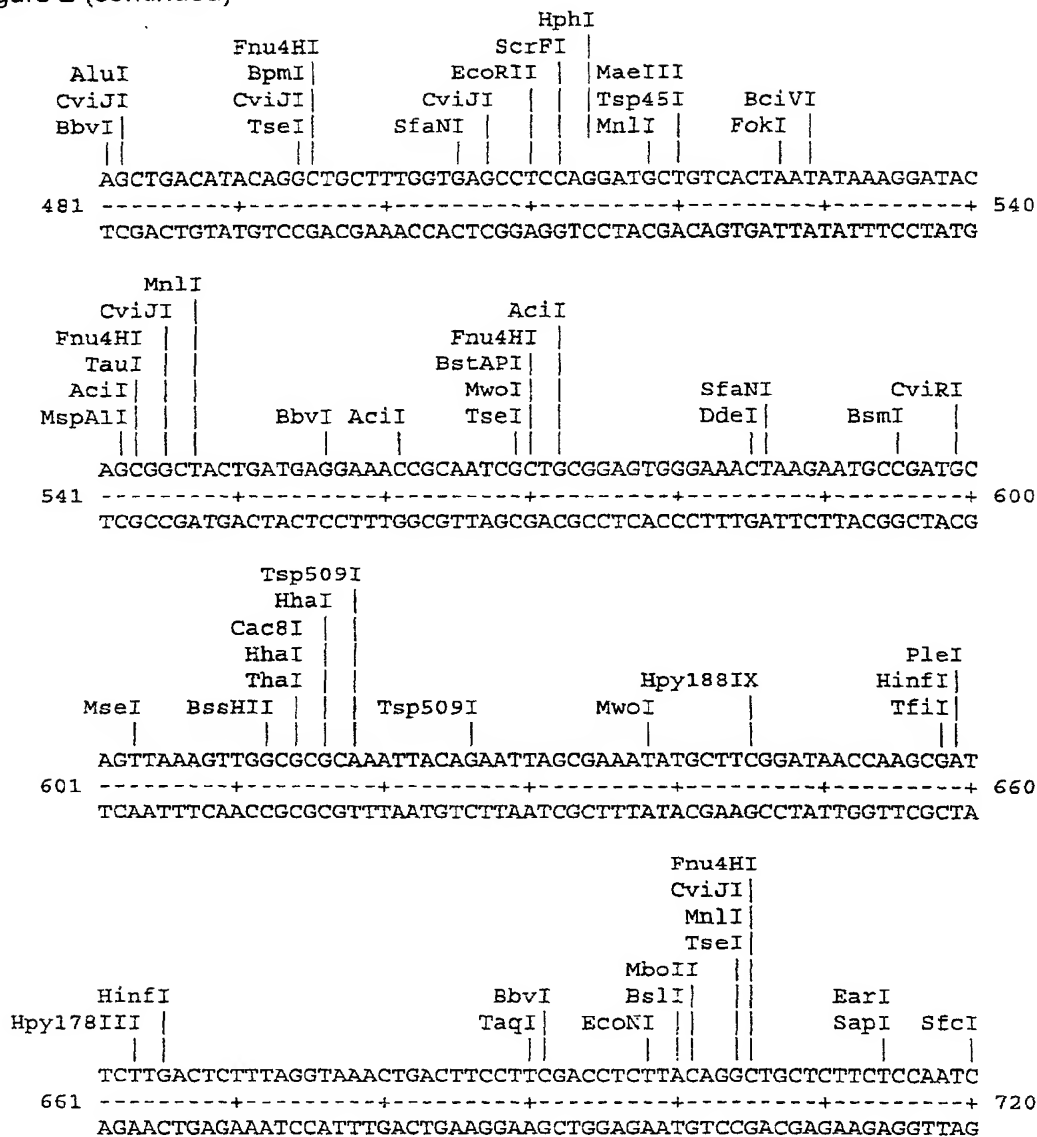


Figure 2 (continued)



T044570 0294T001





Figure 2 (continued)

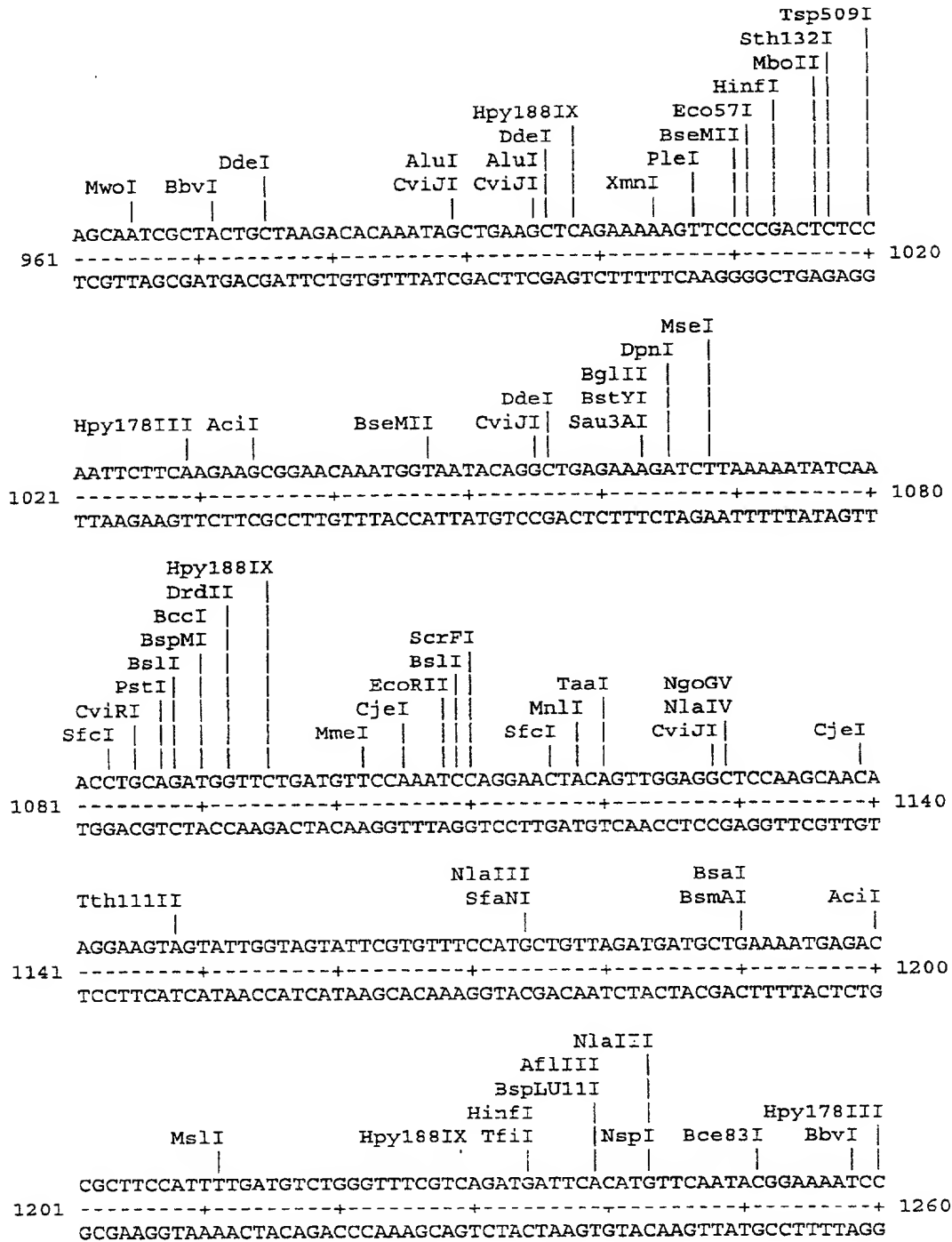




Figure 2 (continued)

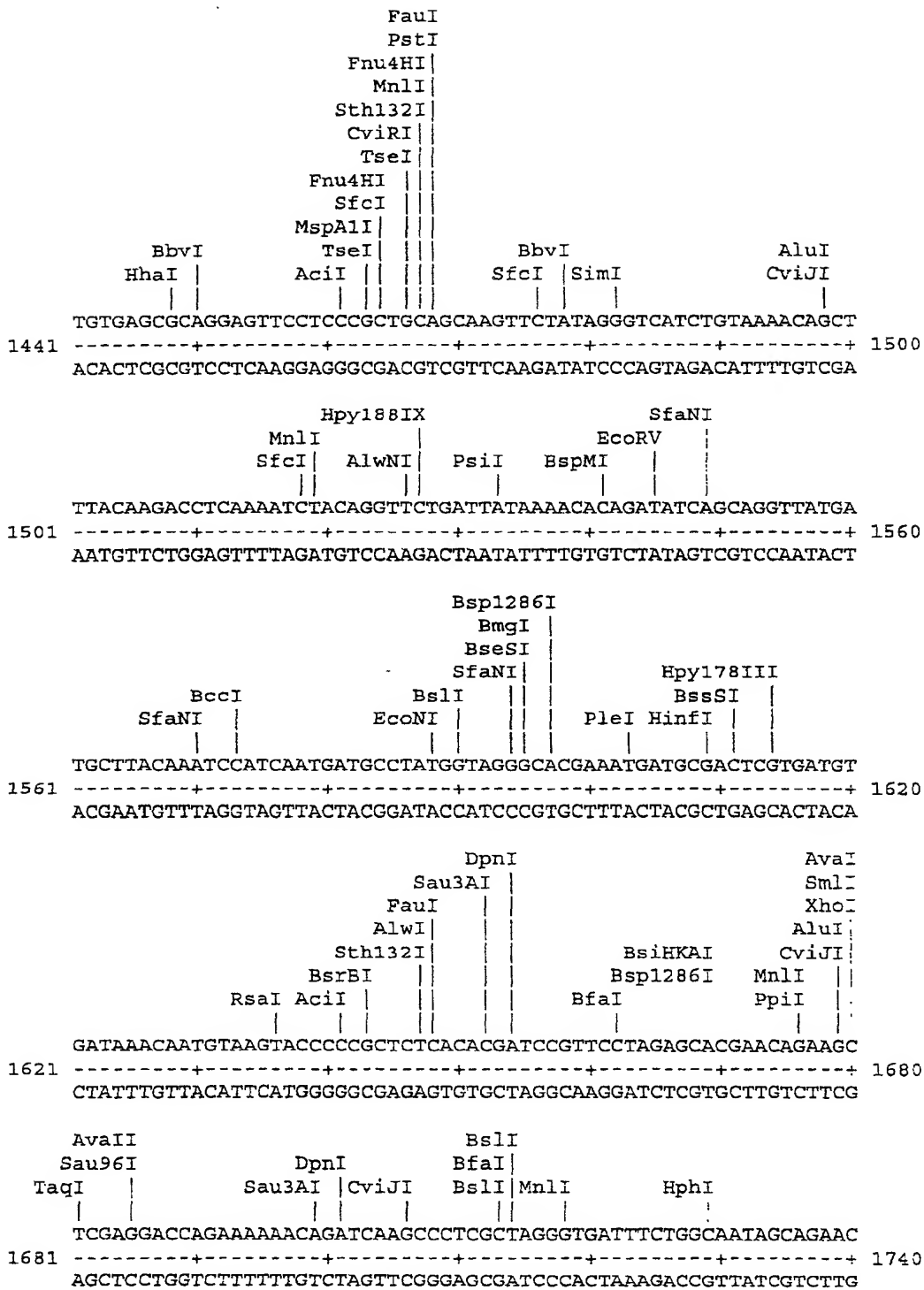


Figure 2 (continued)

SfcI FokI Bce83I DpnI Sau3AI CviRI BsrI TaqI  
 TCTTGGAGATGTCTATAGTCAAGTTTCGGCACTACAATCTGTAATGCAGATCATCCAGTC  
 1741 -----+----- 1800  
 AGAACCTCTACAGATATCAGTTCAAAGCCGTGATGTTAGACATTACGTCTAGTAGGTCAG

HinfI MnlI Hpy188IX DpnI BseRI AluI CviJI BtsI MaeIII Tsp45I  
 TfiI SmlI MnlI Sau3AI HindIII TspRI CviJI BsaXI Hin4I  
 GAATCCTCAAGCGAATAATGAGGAGATCAGACAAAAGCTTACATCGGCAGTGACAAAGCC  
 1801 -----+----- 1860  
 CTTAGGAGTTCGCTTATTACTCCTCTAGTCTGTTTTCGAATGTAGCCGTCACGTGTTTCGG

CviJI MnlI BslI PflMI TaaI CviRI PleI HinfI AluI CviJI  
 TCCACAGTTTGGCTATCCTTATGTGCAACTTTCTAATGACTCTACACAGAAGTTCATAGC  
 1861 -----+----- 1920  
 AGGTGTCAAACCGATAGGAATACAGCTTGAAAGATTACTGAGATGTGTCTTCAAGTATCG

Tth111III Tsp509I BfaI DpnI BstYI Sau3AI AlwI Fnu4HI TseI PvuII MspAII Eco57I AluI AlwNI CviJI  
 TAAATTAGAAAGTTTGTGTTGCTGAAGGATCTAGGACAGCAGCTGAAATAAAAGCACTTTC  
 1921 -----+----- 1980  
 ATTTAATCTTTCAAACAAACGACTTCCTAGATCCTGTGTCGACTTTATTTTCGTGAAAG

BspMI AlwNI AarI CviJI  
 CTTTGAAACGAACTCCTTGTGTTTATTGAGGAGGTGCTGGTCAATATCGGCTCTCTATATTC  
 1981 -----+----- 2040  
 GAAACTTTGCTTGAGGAACAAATAAGTCGTCCACGACCAGTTATAGCCGAGAGATATAAG

T004460-12401

Figure 2 (continued)

```

                MslI
                DdeI
                BsbI
                |
                |
TGGTTATCTCCAATAACAACACCTAAGTGTTCGTTTGGAGAGATTATTATGTGCTTTGGT
2041 -----+-----+-----+-----+-----+ 2100
ACCAATAGAGGTTATTGTTGTGGATTCACAAGCAAACCTCTCTAATAATACACGAAACCA

MnlI
CviJI |      CviJI      DpnI
HaeI  |      HaeI      Sau3AI
HaeIII|      HaeIII    MboII
StuI  |      StuI      BsbI BfaI
                |
AAGGCCTTTGTTGAGGCCTTACCAACACACTAGAACGATCTTCAATAAATAAAAGA
2101 -----+-----+-----+-----+-----+ 2156
TTCCGGAAACAACCTCCGGAATGGTTGTGTGATCTTGCTAGAAGTTATTTATTTCT

```

10014670-13401

atgacaaaaa	aacattatgc	ttgggttgta	gaagggatcc	tcaatcgttt	gcctaaacag	60
ttttttgtga	aatgtagtgt	tgtcgactgg	aacacattcg	ttccttcaga	aacctccact	120
acagaaaaag	ctgctacaaa	cgctatgaaa	tacaaatact	gtgtttggca	gtggctcgtc	180
ggaaagcata	gtcaggttcc	ttggatcaat	ggacagaaaa	agcctctata	tctttatgga	240
gctttcttaa	tgaacccttt	agcaaaggct	acgaagacta	cgtaaagtgg	aaaagaaaac	300
ctagcttggt	ttattggagg	aactttaggg	ggactcagaa	aagctggaga	ctggctcgcc	360
acagtacgtt	atgagtatgt	cgaagccttg	tcggttccag	aaatagatgt	ttcagggatt	420
ggcctgggta	atttattaaa	gttttgggtc	gcccaagcaa	ttgctgctaa	ctatgatcct	480
aaagaggcta	atggttttac	aaattataaa	ggattttccg	ctctatatat	gtatggcatc	540
acagattctc	tatcattcag	agcttatggg	gcttactcca	aaccagcaaa	cgataaaactc	600
ggcagtgatt	ttactttccg	aaagtttgat	ctaggtataa	tttcagcgtt	<u>taa</u> agtcaaa	660
ttttaataaa	atctttaaaa	acaggctcgc	attaattatt	agtgagagct	ttttttttat	720
tttttataat	aaaactaaaa	gattttttatt	attttttgag	ttttt atg gtt aat cct		777
				Met Val Asn Pro		
				1		
att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat	825					
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp						
5 10 15 20						
ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa	873					
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu						
25 30 35						
gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc	921					
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr						
40 45 50						
gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc	969					
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu						
55 60 65						
atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct	1017					
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser						
70 75 80						
tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct	1065					
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Thr Ala Thr Ala Pro						
85 90 95 100						

Figure 3 (continued)

acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	1113
Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	
105 110 115	
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct	1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala	
120 125 130	
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg	1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala	
135 140 145	
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat	1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat	1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	
165 170 175 180	
gct tgc gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc	1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac	1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca	1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct	1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	
230 235 240	
aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
245 250 255 260	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
265 270 275	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
280 285 290	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
295 300 305	

Figure 3 (continued)

ctt	caa	gaa	gcg	gaa	caa	atg	gta	ata	cag	gct	gag	aaa	gat	ctt	aaa	1737
Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	Lys	Asp	Leu	Lys	
	310					315					320					
aat	atc	aaa	cct	gca	gat	ggc	tct	gat	gtt	cca	aat	cca	gga	act	aca	1785
Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	Pro	Gly	Thr	Thr	
325					330					335					340	
gtt	gga	ggc	tcc	aag	caa	caa	gga	agt	agt	att	ggc	agt	att	cgt	gtt	1833
Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	Ser	Ile	Arg	Val	
				345					350					355		
tcc	atg	ctg	tta	gat	gat	gct	gaa	aat	gag	acc	gct	tcc	att	ttg	atg	1881
Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	Ser	Ile	Leu	Met	
			360					365						370		
tct	ggg	ttt	cgt	cag	atg	att	cac	atg	ttc	aat	acg	gaa	aat	cct	gat	1929
Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	Glu	Asn	Pro	Asp	
	375					380						385				
tct	caa	gct	gcc	caa	cag	gag	ctc	gca	gca	caa	gct	aga	gca	gcg	aaa	1977
Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	Arg	Ala	Ala	Lys	
	390					395					400					
gcc	gct	gga	gat	gac	agt	gct	gct	gca	gcg	ctg	gca	gat	gct	cag	aaa	2025
Ala	Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Asp	Ala	Gln	Lys	
405					410					415				420		
gct	tta	gaa	gcg	gct	cta	ggc	aaa	gct	ggg	caa	caa	cag	ggc	ata	ctc	2073
Ala	Leu	Glu	Ala	Ala	Leu	Gly	Lys	Ala	Gly	Gln	Gln	Gln	Gly	Ile	Leu	
				425					430					435		
aat	gct	tta	gga	cag	atc	gct	tct	gct	gct	gtt	gtg	agc	gca	gga	gta	2121
Asn	Ala	Leu	Gly	Gln	Ile	Ala	Ser	Ala	Ala	Val	Val	Ser	Ala	Gly	Val	
			440					445					450			
ctc	ccg	ctg	cag	caa	gtt	cta	tgg	atc	cga	gct	cgg	tac	caa	gct	tac	2169
Leu	Pro	Leu	Gln	Gln	Val	Leu	Trp	Ile	Arg	Ala	Arg	Tyr	Gln	Ala	Tyr	
		455					460					465				
gta	gaa	caa	aaa	ctc	atc	tca	gaa	gag	gat	ctg	aat	agc	gcc	gtc	gac	2217
Val	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	
	470					475					480					
cat	cat	cat	cat	cat	cat	tga										2238
His	His	His	His	His	His											
485					490											



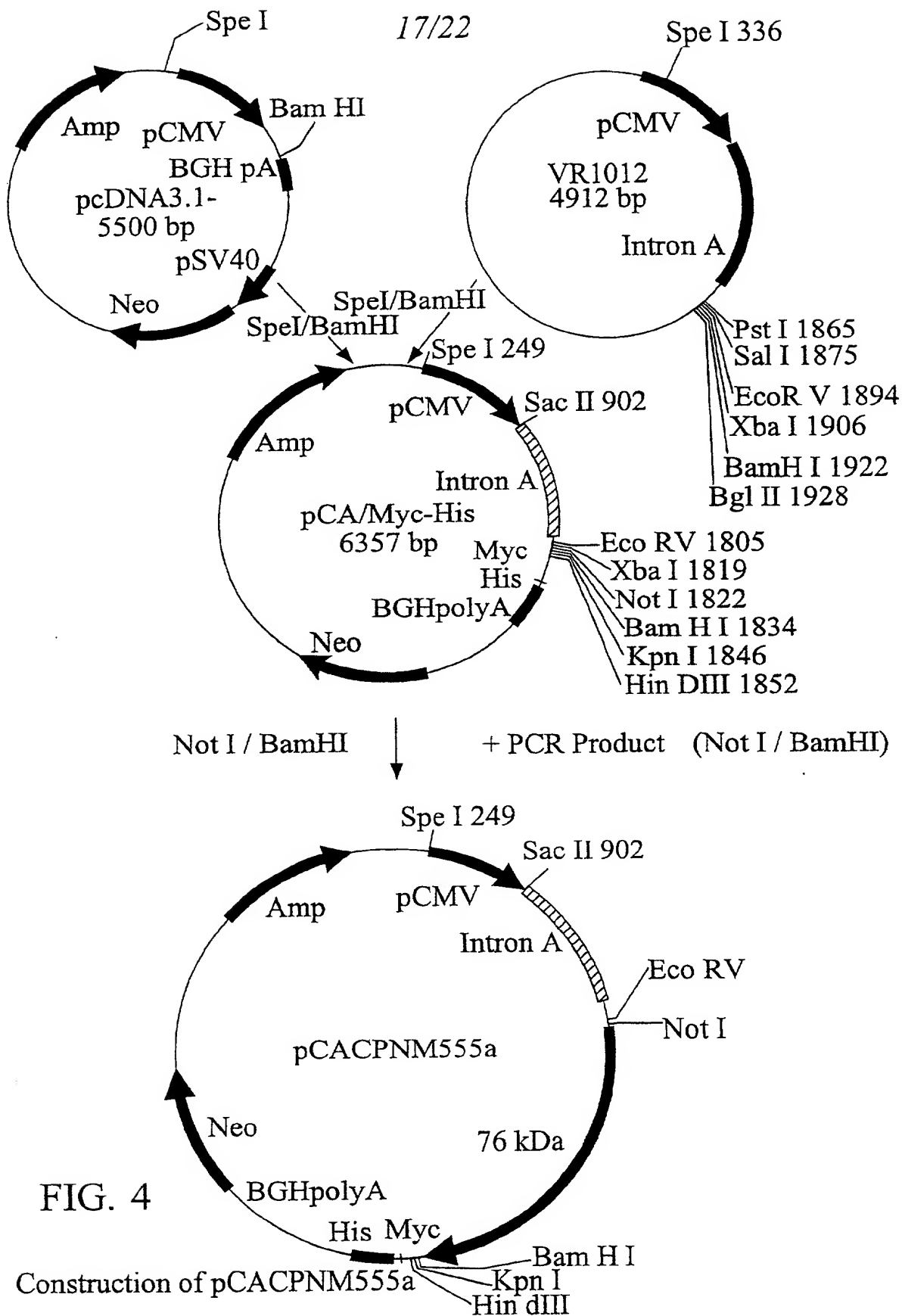


FIG. 4

Construction of pCACPNM555a

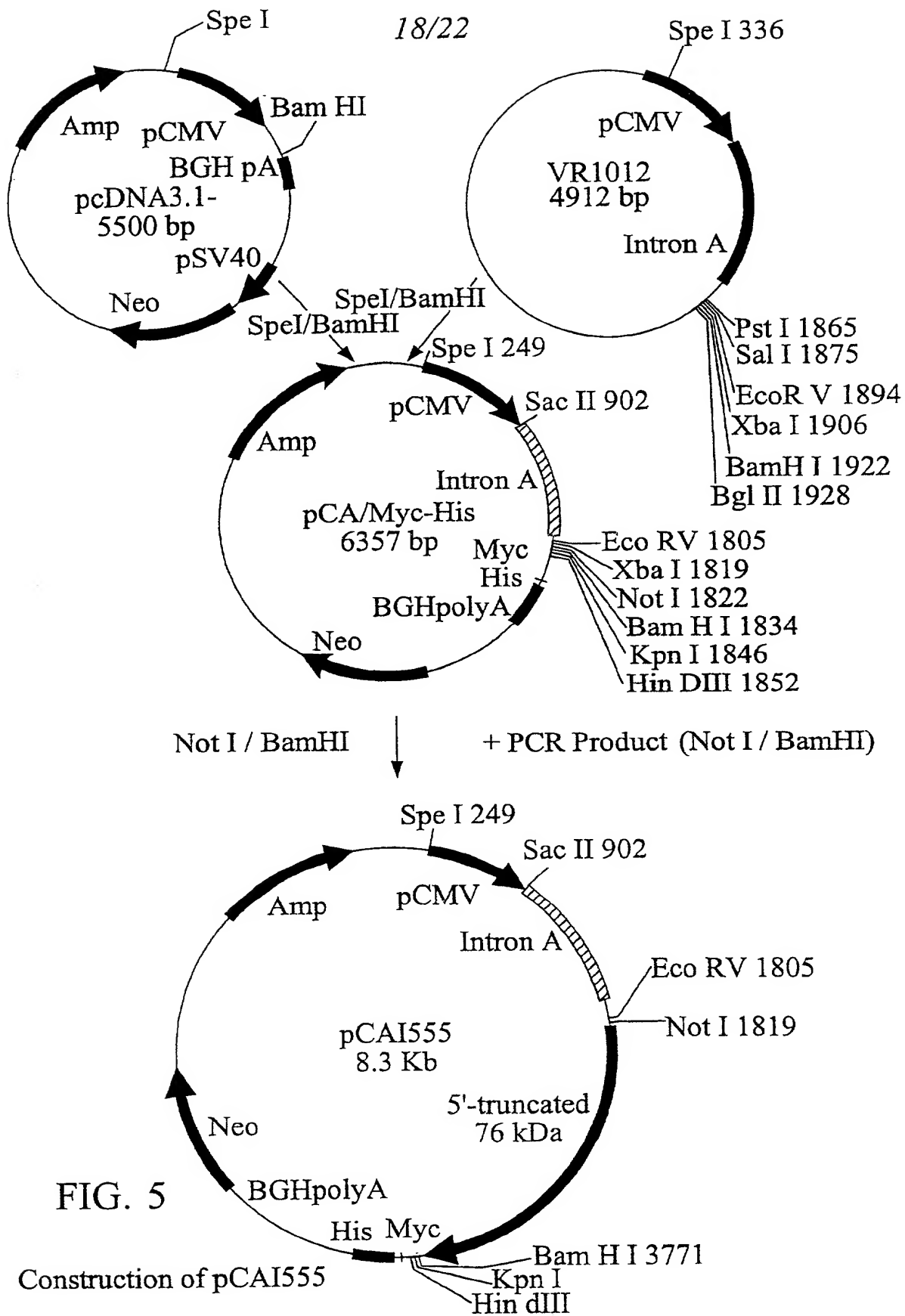


FIG. 5

Construction of pCAI555

FIG. 6

### Construction of pCAD76kDa

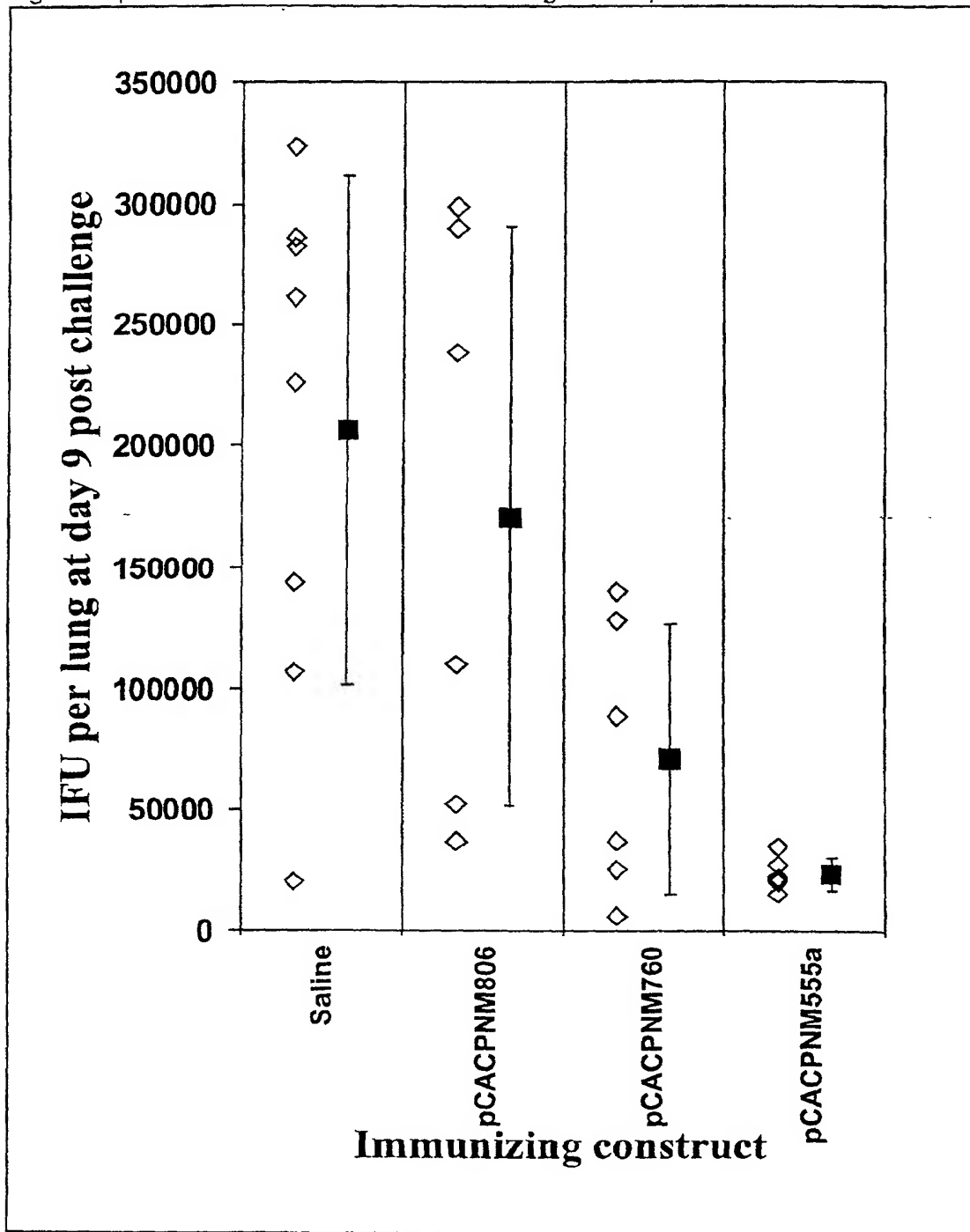
Figure 7: pCACPNM555a Confers Protection Against *C. pneumoniae* Infection .

Figure 8: pCAI555 Confers Protection Against *C. pneumoniae* Infection.

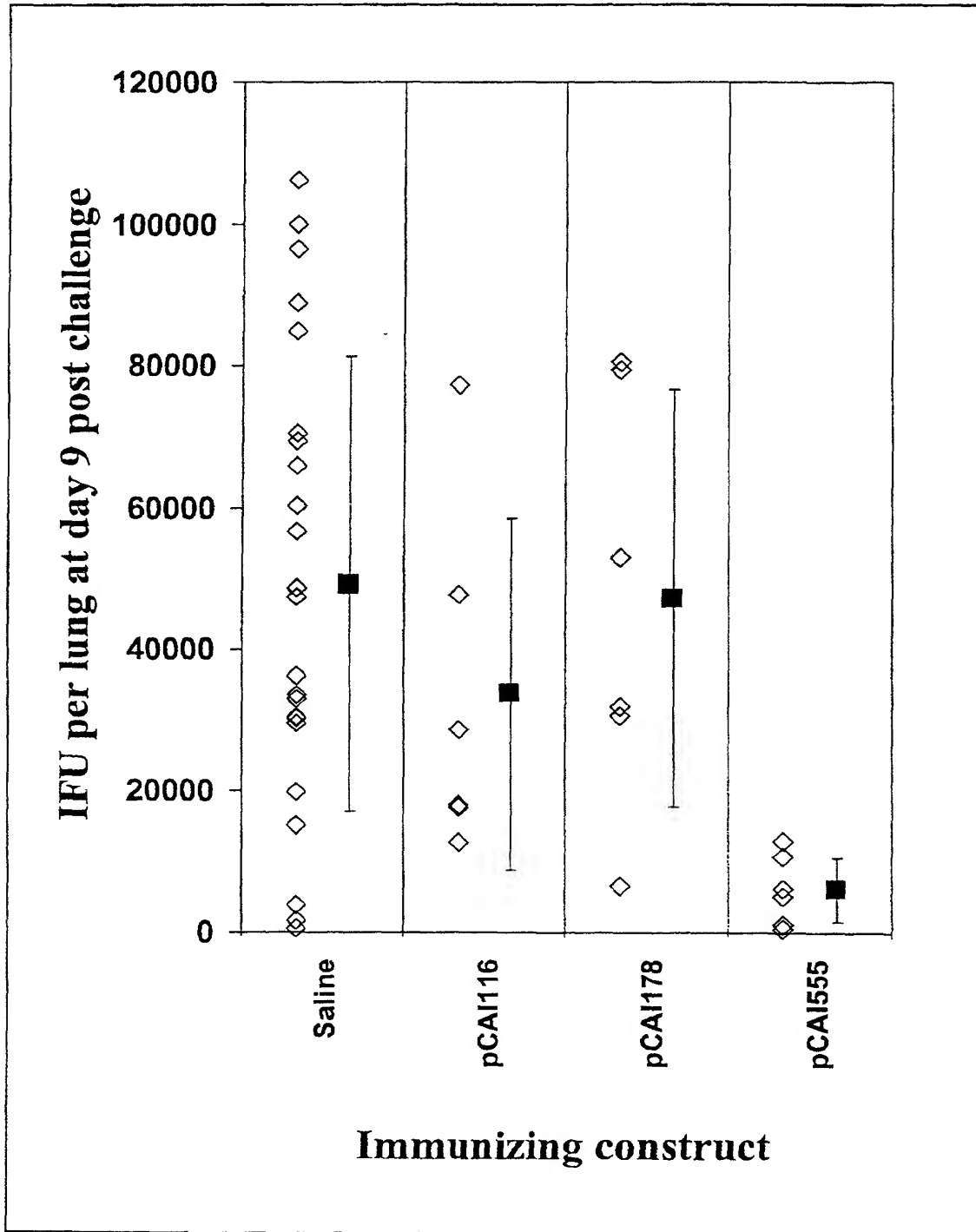
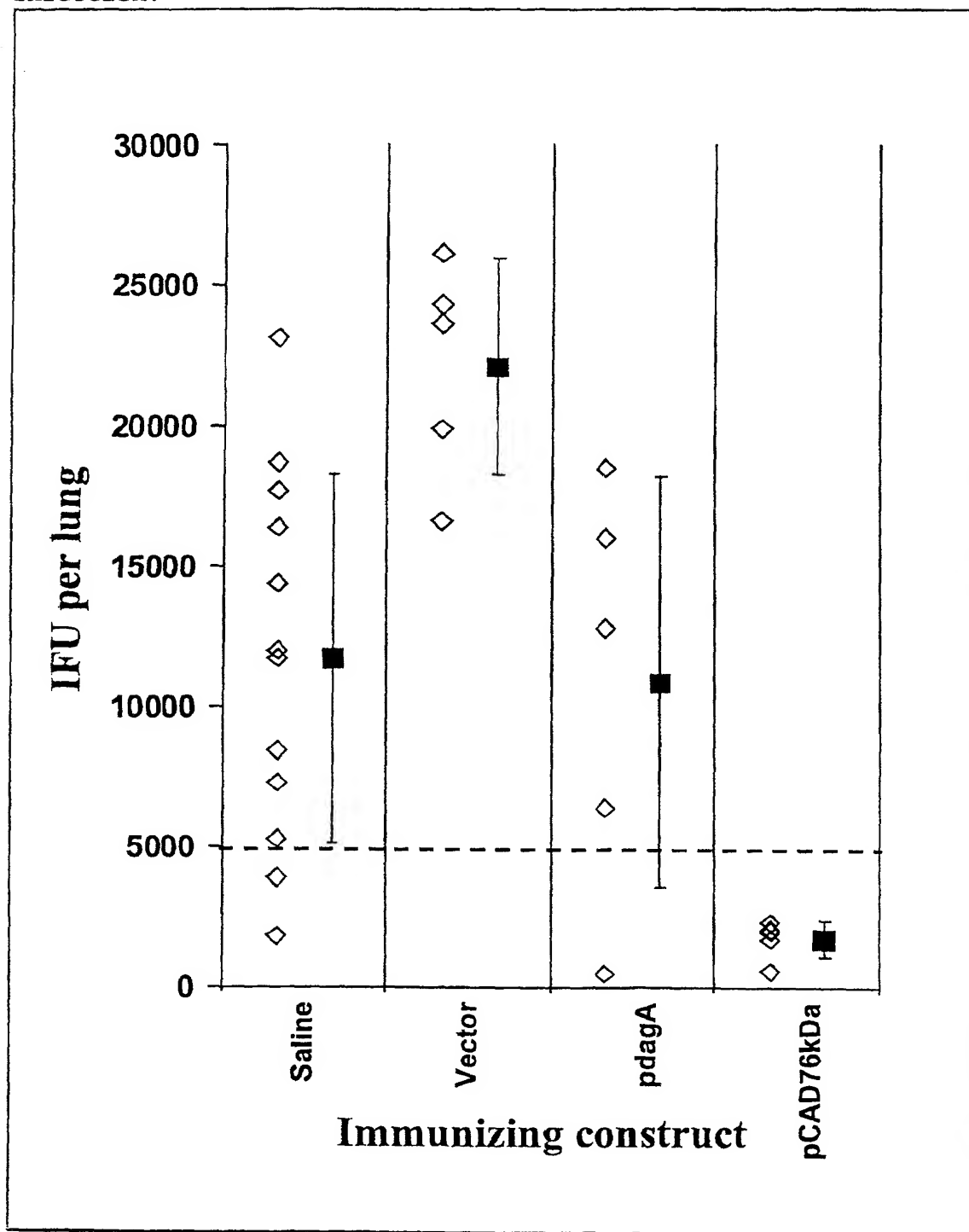


Figure 9: pCAD76kDa Confers Protection against *C. pneumoniae* Infection.



## SEQUENCE LISTING

<110> Aventis Pasteur Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-13

<140>

<141>

<150> US 60/132,270

<151> 1999-05-03

<150> US 60/141,276

<151> 1999-06-30

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 2156

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (101)..(2053)

<400> 1

ataaaatctt taaaaacagg ctgcgattaa ttattagtga gagctttttt tttatttttt 60

ataataaaaac taaaagattt ttattatttt ttgagttttt atg gtt aat cct att 115  
Met Val Asn Pro Ile  
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163  
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu  
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211  
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala  
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259  
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp  
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307  
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met  
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355  
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser  
70 75 80 85

Footnote 0/94Foot

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg	403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr	
90 95 100	
cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct	451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala	
105 110 115	
tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct	499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala	
120 125 130	
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct	547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala	
135 140 145	
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc	595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala	
150 155 160 165	
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct	643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala	
170 175 180	
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc	691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe	
185 190 195	
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	



3/22

caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345 350 355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360 365 370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375 380 385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390 395 400 405	
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410 415 420	
tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425 430 435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct	1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro	
440 445 450	
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag	1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys	
455 460 465	
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt	1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly	
470 475 480 485	
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat	1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn	
490 495 500	
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca	1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr	
505 510 515	
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca	1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr	
520 525 530	

1001450-1401

4/22

gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga 1747  
 Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly  
 535 540 545

gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc 1795  
 Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile  
 550 555 560 565

cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca 1843  
 Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr  
 570 575 580

tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt 1891  
 Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu  
 585 590 595

tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt 1939  
 Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe  
 600 605 610

gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa 1987  
 Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu  
 615 620 625

acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta 2035  
 Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu  
 630 635 640 645

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 2083  
 Tyr Ser Gly Tyr Leu Gln  
 650

ttattatgtg ctttggttaag gcctttgttg aggccttacc aacacactag aacgatcttc 2143

aataaataaa aga 2156

<210> 2  
 <211> 651  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 2  
 Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
 1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
 20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
 35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
 50 55 60

1004460-1440

5/22

Val	Asn	Ala	Leu	Met	Ser	Leu	Ala	Asp	Lys	Leu	Gly	Ile	Ala	Ser	Ser	65	70	75	80
Asn	Ser	Ser	Ser	Ser	Thr	Ser	Arg	Ser	Ala	Asp	Val	Asp	Ser	Thr	Thr	85	90	95	
Ala	Thr	Ala	Pro	Thr	Pro	Pro	Pro	Pro	Thr	Phe	Asp	Asp	Tyr	Lys	Thr	100	105	110	
Gln	Ala	Gln	Thr	Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	115	120	125	
Asp	Ile	Gln	Ala	Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	130	135	140	
Lys	Asp	Thr	Ala	Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	145	150	155	160
Glu	Thr	Lys	Asn	Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	165	170	175	
Leu	Ala	Lys	Tyr	Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	180	185	190	
Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	195	200	205	
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	210	215	220	
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	225	230	235	240
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	245	250	255	
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	260	265	270	
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	275	280	285	
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	290	295	300	
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	305	310	315	320
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	325	330	335	
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	340	345	350	

10014670-121491

6/22

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala		
355	360	365
Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr		
370	375	380
Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala		
385	390	395 400
Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala		
	405	410 415
Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln		
	420	425 430
Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val		
	435	440 445
Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val		
	450	455 460
Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr		
	465	470 475 480
Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr		
	485	490 495
Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser		
	500	505 510
Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg		
	515	520 525
Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn		
	530	535 540
Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser		
	545	550 555 560
Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile		
	565	570 575
Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr		
	580	585 590
Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys		
	595	600 605
Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys		
	610	615 620
Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val		
	625	630 635 640

10014570-121401

7/22

Asn Ile Gly Ser Leu Tyr Ser Gly Tyr Leu Gln  
645 650

<210> 3  
<211>  
<212> DNA  
<213> Chlamydia pneumoniae  
<220> 1842  
<221> CDS  
<222> (101..(2053)

<400> 3  
atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct 48  
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser  
1 5 10 15  
tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct 96  
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro  
20 25 30  
acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca 144  
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr  
35 40 45  
gct tac gat act atc ttg acc tca aca tca cta gct gac ata cag gct 192  
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala  
50 55 60  
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg 240  
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala  
65 70 75 80  
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat 288  
Ala Thr Asp Glu Thr Ala Ile Ala Glu Trp Glu Thr Lys Asn  
85 90 95  
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat 336  
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr  
100 105 110  
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc 384  
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser  
115 120 125  
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac 432  
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn  
130 135 140  
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca 480  
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro  
145 150 155 160  
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct 528  
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala  
165 170 175

10011670-10011670

8/22

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	576
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
180 190 195	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	624
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
200 205 210	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	672
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
215 220 225	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	720
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
230 235 240 245	
ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa	768
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys	
250 255 260	
aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca	816
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr	
265 270 275	
gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt	864
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val	
280 285 290	
tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg	912
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met	
295 300 305	
tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat	960
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp	
310 315 320 325	
tct caa gct gcc caa cag gag ctg gca gca caa gct aga gca gcg aaa	1008
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys	
330 335 340	
gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa	1056
Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys	
345 350 355	
gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctg	1104
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu	
360 365 370	
aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt	1152
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val	
375 380 385	
Cct ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac	1200
Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr	
390 395 400 405	

10014670-121401

9/22

aag acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca 1248  
 Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala  
 410 415 420

ggt tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga 1296  
 Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg  
 425 430 435

aat gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc 1344  
 Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu  
 440 445 450

aca cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa 1392  
 Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys  
 455 460 465

aca gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt 1440  
 Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu  
 470 475 480 485

gga gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc 1488  
 Gly Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile  
 490 495 500

act cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt 1536  
 Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu  
 505 510 515

aca tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa 1584  
 Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln  
 520 525 530

ctt tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg 1632  
 Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu  
 535 540 545

ttt gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt 1670  
 Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe  
 550 555 560 565

gaa acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct 1718  
 Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser  
 570 575 580

cta tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 1769  
 Leu Tyr Ser Gly Tyr Leu Gln  
 585

ttattatgtg ctttggtgtaag gcctttgttg aggccttacc aacacactag aacgatcttc 1829

aataaataaaa aga 1842

10014570-121401

10/22

<210> 4

<211> 583

<212> PRT

<213> Chlamydia pneumoniae

<400> 4

Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser  
1 5 10 15  
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro  
20 25 30  
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr  
35 40 45  
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala  
50 55 60  
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala  
65 70 75 80  
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn  
85 90 95  
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr  
100 105 110  
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser  
115 120 125  
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn  
130 135 140  
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro  
145 150 155 160  
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala  
165 170 175  
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr  
180 185 190  
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn  
195 200 205  
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala  
210 215 220  
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile  
225 230 235 240  
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys  
245 250 255

10044570-124401



11/22

Asn Ile Lys	Pro Ala Asp	Gly Ser Asp	Val Pro Asn	Pro Gly Thr	Thr
260		265		270	
Val Gly Gly	Ser Lys Gln	Gln Gly Ser	Ser Ile Gly	Ser Ile Arg	Val
275		280		285	
Ser Met Leu	Leu Asp Asp	Ala Glu Asn	Glu Thr Ala	Ser Ile Leu	Met
290		295		300	
Ser Gly Phe	Arg Gln Met	Ile His Met	Phe Asn Thr	Glu Asn Pro	Asp
305		310		315	320
Ser Gln Ala	Ala Gln Gln	Glu Leu Ala	Ala Gln Ala	Arg Ala Ala	Lys
	325		330		335
Ala Ala Gly	Asp Asp Ser	Ala Ala Ala	Ala Leu Ala	Asp Ala Gln	Lys
	340		345		350
Ala Leu Glu	Ala Ala Leu	Gly Lys Ala	Gly Gln Gln	Gln Gly Ile	Leu
	355		360		365
Asn Ala Leu	Gly Gln Ile	Ala Ser Ala	Ala Val Val	Ser Ala Gly	Val
	370		375		380
Pro Pro Ala	Ala Ala Ser	Ser Ser Ile	Gly Ser Ser	Val Lys Gln	Leu Tyr
385		390		395	400
Lys Thr Ser	Lys Ser Thr	Gly Ser Asp	Tyr Lys Thr	Gln Ile Ser	Ala
	405		410		415
Gly Tyr Asp	Ala Tyr Lys	Ser Ile Asn	Asp Ala Tyr	Gly Arg Ala	Arg
	420		425		430
Asn Asp Ala	Thr Arg Asp	Val Ile Asn	Asn Val Ser	Thr Pro Ala	Leu
	435		440		445
Thr Arg Ser	Val Pro Arg	Ala Arg Thr	Glu Ala Arg	Gly Pro Glu	Lys
	450		455		460
Thr Asp Gln	Ala Leu Ala	Arg Val Ile	Ser Gly Asn	Ser Arg Thr	Leu
465		470		475	480
Gly Asp Val	Tyr Ser Gln	Val Ser Ala	Leu Gln Ser	Val Met Gln	Ile
	485		490		495
Ile Gln Ser	Asn Pro Gln	Ala Asn Asn	Glu Glu Ile	Arg Gln Lys	Leu
	500		505		510
Thr Ser Ala	Val Thr Lys	Pro Pro Gln	Phe Gly Tyr	Pro Tyr Val	Gln
	515		520		525
Leu Ser Asn	Asp Ser Thr	Gln Lys Phe	Ile Ala Lys	Leu Glu Ser	Leu
530		535		540	

10614670-13444

12/22

Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe  
545 550 555 560

Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser  
565 570 575

Leu Tyr Ser Gly Tyr Leu Gln  
580

<210> 5

<211> 1456

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (101)..(1456)

<400> 5

ataaaatctt taaaaacagg ctgcgattaa ttattagtga gagctttttt ttattttttt 60

ataataaaac taaaagattt ttattttttt ttgagttttt atg gtt aat cct att 115  
Met Val Asn Pro Ile  
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163  
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu  
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211  
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala  
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259  
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp  
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307  
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met  
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355  
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser  
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403  
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr  
90 95 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451  
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala  
105 110 115

1001456-121401

13/22

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct	499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala	
120 125 130	
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct	547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala	
135 140 145	
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc	595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala	
150 155 160 165	
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct	643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala	
170 175 180	
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc	691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe	
185 190 195	
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	
caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	

10044670-121404

14/22

gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc 1171  
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser  
345 350 355

atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct 1219  
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser  
360 365 370

ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct 1267  
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser  
375 380 385

caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc 1315  
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala  
390 395 400 405

gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct 1363  
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala  
410 415 420

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat 1411  
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn  
425 430 435

gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta 1456  
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val  
440 445 450

<210> 6

<211> 452

<212> PRT

<213> Chlamydia pneumoniae

<400> 6

Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser  
65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr  
85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr  
100 105 110

1004670-1440

15/22

Gln	Ala	Gln	Thr	Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	
		115						120				125				
Asp	Ile	Gln	Ala	Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	
	130					135					140					
Lys	Asp	Thr	Ala	Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	
	145				150					155					160	
Glu	Thr	Lys	Asn	Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	
			165						170					175		
Leu	Ala	Lys	Tyr	Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	
			180					185					190			
Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	
		195					200					205				
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	
	210					215					220					
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	
	225				230					235					240	
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	
			245						250					255		
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	
		260					265						270			
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	
		275					280					285				
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	
	290					295					300					
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	
	305				310					315					320	
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	
			325						330					335		
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	
		340						345						350		
Ser	Ile	Arg	Val	Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	
		355					360					365				
Ser	Ile	Leu	Met	Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	
	370					375					380					
Glu	Asn	Pro	Asp	Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	
	385				390					395					400	

10014670-1E1401

16/22

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala  
405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln  
420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val  
435 440 445

Ser Ala Gly Val  
450

<210> 7  
<211> 2238  
<212> DNA  
<213> Chlamydia pneumoniae

<220>  
<221> CDS  
<222> (766) .. (2235)

<400> 7  
atgacaaaaa aacattatgc ttgggttgta gaagggatc tcaatcgttt gcctaaacag 60  
ttttttgtga aatgtagtgt tgtcgactgg aacacattcg ttcccttcaga aacctccact 120  
acagaaaaag ctgctacaaa cgctatgaaa tacaataact gtgtttggca gtggctcgtc 180  
ggaaagcata gtcaggttcc ttggatcaat ggacagaaaa agcctctata tctttatgga 240  
gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaac 300  
ctagcttggt ttattggagg aactttaggg ggactcagaa aagctggaga ctggctcgcc 360  
acagtacgtt atgagtatgt cgaagccttg tcggttccag aaatagatgt ttcagggatt 420  
ggccgtggta atttattaaa gttttggttc gcccaagcaa ttgctgctaa ctatgatect 480  
aaagaggcta atggttttac aaattataaa ggattttccg ctctatatat gtatggcatc 540  
acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaactc 600  
ggcagtgatt ttactttccg aaagtttgat ctaggataaa tttcagcggt ttaagtcaaa 660  
ttttaataaa atctttaaaa acaggctcgc attaattatt agtgagagct ttttttttat 720  
tttttataat aaaactaaaa gatttttatt attttttgag ttttt atg gtt aat cct 777  
Met Val Asn Pro

1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825  
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp  
5 10 15 20

10014620-164401

17/22

ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa	873
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu	
25 30 35	
gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc	921
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr	
40 45 50	
gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc	969
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu	
55 60 65	
atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct	1017
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser	
70 75 80	
tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct	1065
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro	
85 90 95 100	
acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	1113
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	
105 110 115	
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct	1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala	
120 125 130	
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg	1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala	
135 140 145	
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat	1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat	1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	
165 170 175 180	
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc	1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac	1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca	1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct	1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	
230 235 240	

10014520-2440

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat 1545  
 Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr  
 245 250 255 260

ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat 1593  
 Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn  
 265 270 275

aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct 1641  
 Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala  
 280 285 290

aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att 1689  
 Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile  
 295 300 305

ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa 1737  
 Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys  
 310 315 320

aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca 1785  
 Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr  
 325 330 335 340

gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt 1833  
 Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val  
 345 350 355

tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg 1881  
 Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met  
 360 365 370

tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat 1929  
 Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp  
 375 380 385

tct caa gct gcc caa cag gag ctg gca gca caa gct aga gca gcg aaa 1977  
 Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys  
 390 395 400

gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa 2025  
 Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys  
 405 410 415 420

gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctg 2073  
 Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu  
 425 430 435

aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta 2121  
 Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val  
 440 445 450

10014370-2444



19/22

ctc ccg ctg cag caa gtt cta tgg atc cga gct cgg tac caa gct tac 2169  
 Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr  
 455 460 465

gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac 2217  
 Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp  
 470 475 480

cat cat cat cat cat cat tga 2238  
 His His His His His His  
 485 490

<210> 8  
 <211> 490  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 8  
 Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
 1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
 20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
 35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
 50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser  
 65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr  
 85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr  
 100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala  
 115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile  
 130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp  
 145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu  
 165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly  
 180 185 190

1004460 "134404"

20/22

Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	195	200	205	
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	210	215	220	
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	225	230	235	240
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	245	250	255	
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	260	265	270	
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	275	280	285	
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	290	295	300	
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	305	310	315	320
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	325	330	335	
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	340	345	350	
Ser	Ile	Arg	Val	Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	355	360	365	
Ser	Ile	Leu	Met	Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	370	375	380	
Glu	Asn	Pro	Asp	Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	385	390	395	400
Arg	Ala	Ala	Lys	Ala	Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	405	410	415	
Asp	Ala	Gln	Lys	Ala	Leu	Glu	Ala	Ala	Leu	Gly	Lys	Ala	Gly	Gln	Gln	420	425	430	
Gln	Gly	Ile	Leu	Asn	Ala	Leu	Gly	Gln	Ile	Ala	Ser	Ala	Ala	Val	Val	435	440	445	
Ser	Ala	Gly	Val	Leu	Pro	Leu	Gln	Gln	Val	Leu	Trp	Ile	Arg	Ala	Arg	450	455	460	
Tyr	Gln	Ala	Tyr	Val	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	465	470	475	480

10014670-401401

```
<210> 9
<211> 43
<212> DNA
<213> primer
```

ataagaatgc ggccgccacc atgggtaatc ctattgggcc agg 43

<400> 10

```
<210> 11
<211> 43
<212> DNA
<213> primer
```

ataagaatgc ggccgccacc atgagtctgg cagataagct ggg 43

<400> 12

```
<210> 13
<211> 38
<212> DNA
<213> primer
```

gctctagacc gccatgacaa aaaaacatta tgcttggg 38

22/22

<210> 14  
<211> 28  
<212> DNA  
<213> primer

<400> 14

cgggatccat agaacttgct gcagcggg

28

100344570-1234401